FIGURE 1A

```
-185  GAATTCGGGGGGGGTTCAAGAGATCACTGGGACCAGGCCGTGATCTCTATGCCCGAGTCTCAA
-125  CCCTCAACTGTCACCCCAAGGCACTTGGGACGTCCTGGACAGACCCGAGTCCCGGGAAGCC
-65   CCAGCACTGCCGCTGCCACACTGCCCCTGAGCCCCAAATGGGGGAGTGAGAGGCCATAGCTG
                                                                 -28
-30        MetGlyLeuSerThrValProAspLeuLeuLeuProLeuValLeuLeuLeu
-5    TCTGGCCATGGGCCTCTCCACCCGTGCCCTGCCTGGCCTGCTGCCGCTGGTGCTCCTGGAGCTG
                                +1
-10   LeuValGlyIleTyrProSerGlyValIleLeuGlyLeuValProHisLeuGlyAspArgGlu
55    TTGGTGGGAATATACCCCTCAGGGGTTATTGGACTGGTCCCTCACCTAGGGGACCAGGGAG
                                  ***
10    LysArgAspSerValCysProGlnGlyLysTyrIleHisProGlnAsnAsnSerIleCys
115   AAGAGAGATAGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGC
30    CysThrLysCysHisLysGlyThrTyrLeuTyrAsnAspCysProGlyProGlyGlnAsp
175   TGTACCAAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGCCAGGAT
50    ThrAspCysArgGluCysGluSerGlySerPheThrAlaSerGluAsnHisLeuArgHis
235   ACGGACTGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACAC
70    CysLeuSerCysSerLysCysArgLysGluMetGlyGlnValGluIleSerSerCysThr
295   TGCCTCAGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACA
90    ValAspArgAspThrValCysGlyCysArgLysAsnGlnTyrArgHisTyrTrpSerGlu
355   GTGGACCGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAA
```

FIGURE 1B

```
110  AsnLeuGlnCysPheAsnCysSerLeuCysLeuAsnGlyThrValHisLeuSerCys
415  AACCTTTCCAGTGCTTCAATTGCAGCCTCCTGCCTCAATGGGACCGTGCACCTCCTGC

130  GlnGluLysGlnAsnThrValCysThrCysHisAlaGlyPhePheLeuArgGluAsnGlu
475  CAGGAGAAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAG

150  CysValSerCysSerAsnCysLysLysSerLeuGluCysThrLysLeuCysLeuProGln
535  TGTGTCTCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTGCCTACCCCAG

170  IleGluAsnValLysGlyThrGluAspSerGlyThrThrValLeuLeuProLeuValIle
595  ATTGAGAATGTTAAGGGCACTGAGGACTCAGGCACCACAGTGCTGTTGCCCCTGGTCATT

190  PhePheGlyLeuCysLeuLeuSerLeuLeuPheIleGlyLeuMetTyrArgTyrGlnArg
655  TTCTTTGGTCTTTGCCTTTTATCCCTCCTTTCATTGGTTTAATGTATCGCTACCAACGG

210  TrpLysSerLysLeuTyrSerIleValCysGlyLysSerThrProGluGluLysGlyGlu
715  TGGAAGTCCAAGCTCTACTCCATTGTTTGTGGGAAATCGACACCTGAAAAAGACGGGGAG

230  LeuGluGlyThrThrThrLysProLeuAlaProAsnProSerPheSerProThrProGly
775  CTTGAAGGAACTACTACTAAGCCCCTGGCCCCAAACCCAGCTTCCAGTCCCCACTCCAGGC
```

FIGURE 1C

```
250  PheThrProThrLeuGlyPheThrProSerSerThrPheThrSerSerThr
835  TTCACCCCCACCCTGGGCTTCACCCCCAGTCCCGTGCCCAGTTCCACCTTCACCTCCAGCTCCACC

270  TyrThrProGlyAspCysProAsnPheAlaAlaProArgGluValAlaProProTyr
895  TATACCCCCGGTGACTGTCCCAACTTTGCGGCTCCCCGCAGAGAGGTGGCACCACCCTAT

290  GlnGlyAlaAspProIleLeuAlaThrAlaLeuAlaSerAspProIleProAsnProLeu
955  CAGGGGGCTGACCCCATCCTTGCGACAGCCCTCGCCTCCGACCCCATCCCCAACCCCTT

310  GlnLysTrpGluAspSerAlaHisLysProGlnSerLeuAspThrAspAspProAlaThr
1015 CAGAAGTGGGAGGACAGCGCCCACAAGCCACAGAGCCTAGACACTGACGACCCCGCGACG

330  LeuTyrAlaValValGluAsnValProProLeuArgTrpLysGluPheValArgArgLeu
1075 CTGTACGCCGTGGTGGAGAACGTGCCCCCGTTGCGCTGGAAGGAATTCGTGCGGCGCCTA

350  GlyLeuSerAspHisGluIleAspArgLeuGluLeuGlnAsnGlyArgCysLeuArgGlu
1135 GGGCTGAGCGACCACGAGATCGATCGGCTGGAGCTGCAGAACGGGCGCTGCCTGCGCGAG

370  AlaGlnTyrSerMetLeuAlaThrTrpArgArgArgThrProArgArgGluAlaThrLeu
1195 GCGCAATACAGCATGCTGGCCACCTGGCGCCGGCGCGCCGCGGAGGCCACGCTG

390  GluLeuLeuGlyArgValLeuArgAspMetAspLeuLeuGlyCysLeuGluAspIleGlu
1255 GAGCTGCTGGGACGCGTGCTCCGCGACATGGACCTGCTGGGCTGCCTGGAGGACATCGAG
```

FIGURE 1D

```
410   GluAlaLeuCysGlyProAlaAlaLeuProProAlaProSerLeuLeuArg
1315  GAGGCGGCTTTGCGGCGGCCCTCCCCGGCCGCCCAGTCTTCTCAGATGAGGCTGC
1375  GCCCCTGCGGGCCAGCTCTAAGGACCGTCCTGCGAGATCGCCTTCCAACCCCACTTTTTC
1435  TGGAAAGGAGGGGGTCCTGCAGGGCAAGCAGGAGCTAGCAGCCGCCTACTTGGTGCTAAC
1495  CCCTCGATGTACATAGCTTTTCTCAGCTGCCTGCGCGCCGCCGACAGTCAGCGCTGTGCG
1555  CGCGGAGAGAGGTGCGCCGTGGGCTCAAGAGCCTGAGTGGGTTGCGAGGATGAGGG
1615  ACGCTATGCCTCATGCCCGTTTGGGTGTCCTCACCAGCAAGGCTGCTCGGGGCCCCTG
1675  GTTCGTCCCTGAGCCTTTTCACAGTGCATAAGCAGTTTTTTTGTTTTTGTTTTGTTTT
1735  GTTTTGTTTTAAATCAATCATGTTACACTAATAGAAACTTGGCACTCCTGTGCCCCTG
1795  CCTGGACAAGCACATAGCAAGCTGAACTGTCCTAAGGCAGGGGCGAGCACGGAACAATGG
1855  GGCCTTCAGCTGGAGCTGTGGGACTTTTGTACATACACTAAAAATTCTGAAGTTAAAAAAA
1915  AACCCGAATTC
```

Figure 2A

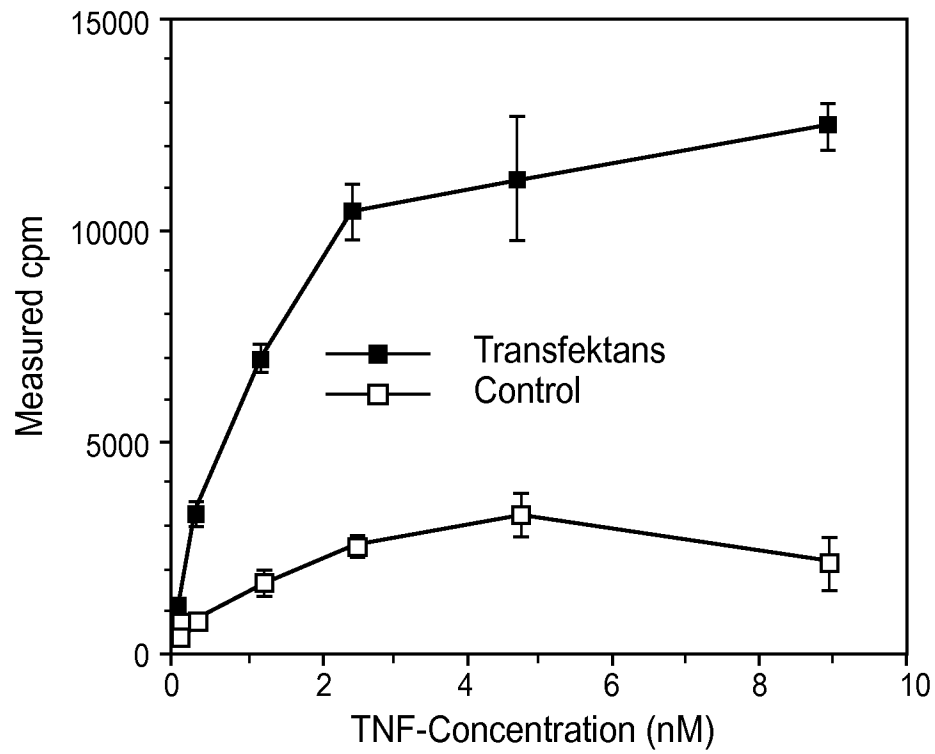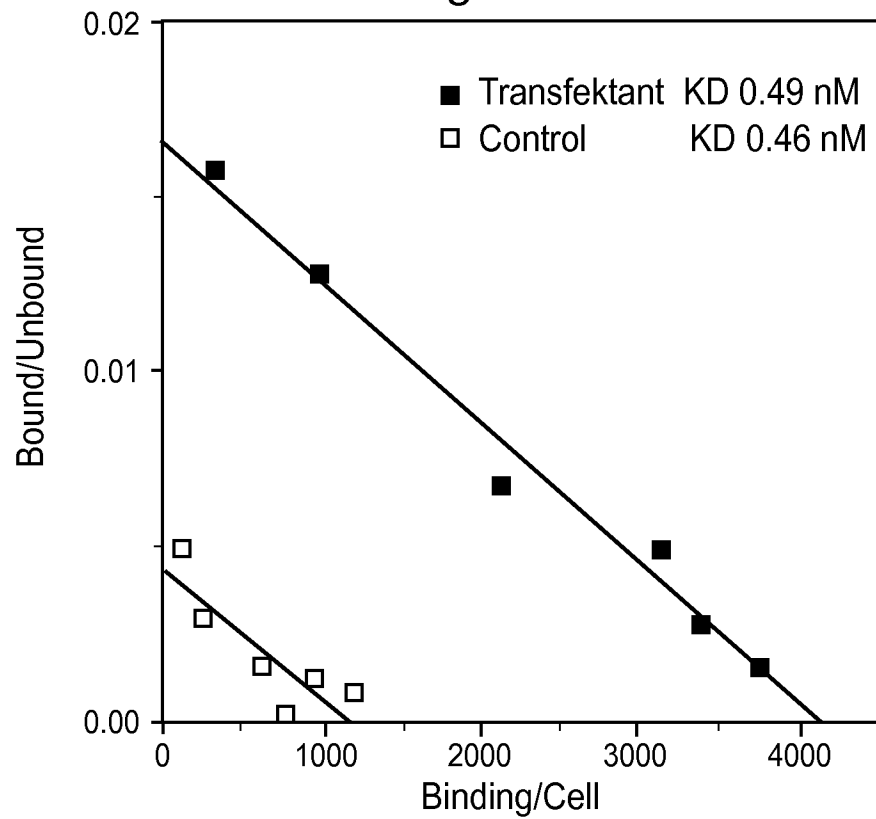## Figure 2B

Figure 3

Sandwich - Assay
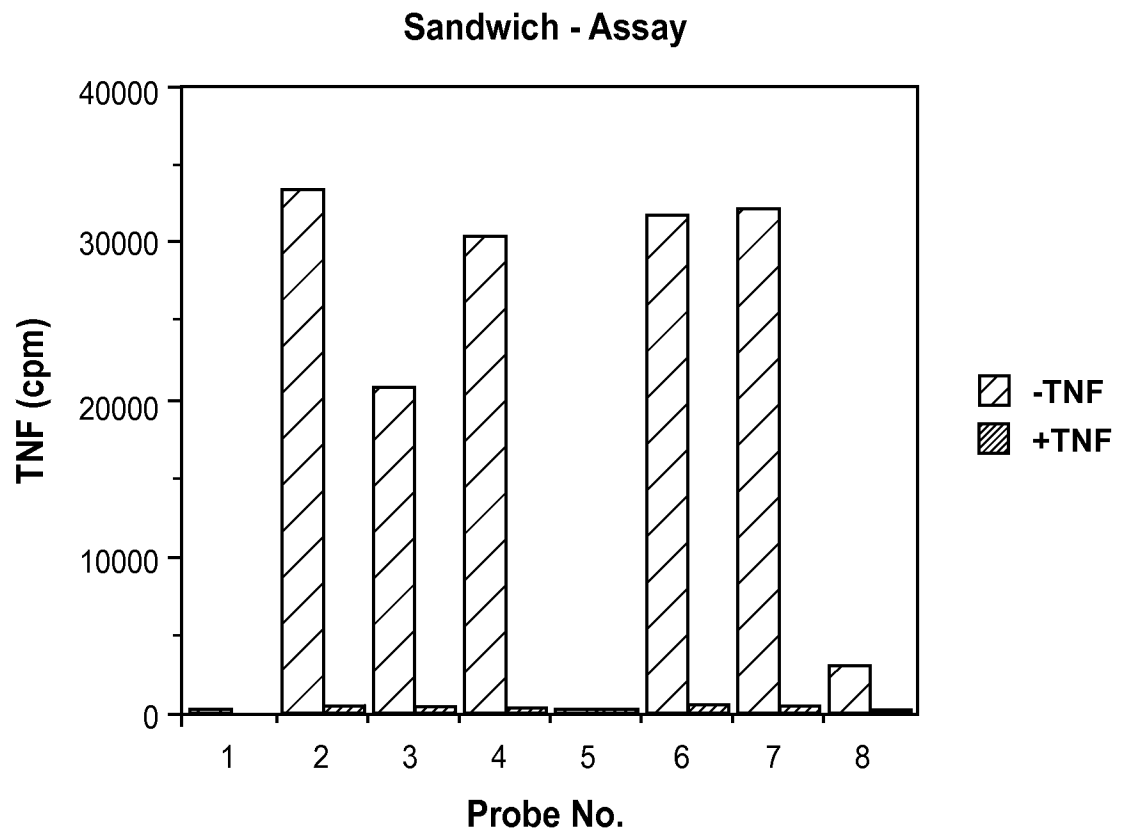
FIGURE 4A

```
  1   SerSerValCysAspSerGluAspSerThrTyrThrThrGlnLeuTrpAsnTrpVal
  1   TCGGACTCCGTGTGTGACTCCGAGGACCAGCACATACACCACCCAGCTCTGGAACTGGGTT

 21   ProGluCysLeuSerCysGlySerArgCysSerSerAspGlnValGluThrGlnAlaCys
 61   CCCGAGTGCTTGAGCTGTGGCTCCCGCTGTAGCTCTGACCAGGTCGAAACTCAAGCCTGC

 41   ThrArgGluGlnAsnArgIleCysThrCysArgProGlyTrpTyrCysAlaLeuSerLys
121   ACTCGGGAACAGAACCGCATCTGCACCTGCAGGCCCGGCTACTGCGCGCTGAGCAAG

 61   GlnGluGlyCysArgLeuCysAlaProLeuArgLysCysArgProGlyPheGlyValAla
181   CAGGAGGGGTGCCGGCTGTGCGCGCCGCTGCGCAAGTGCCGCCCGGGCTTCGGCGTGGCC

 81   ArgProGlyThrGluThrSerAspValValCysLysProCysAlaProGlyThrPheSer
241   AGACCAGGAACTGAAACATCAGAACGTGGTGTGCAAGCCCTGCGCCCCGGGGACGTTCTCC

101   AsnThrThrSerThrAspIleCysArgProHisGlnIleCysAsnValValAlaAlaIle
301   AACACGACTTCATCCACGGATATTTGCAGGCCCCACCAGATCTGTAACGTGGTGGCCATC

121   ProGlyAsnAlaSerArgAspAlaValCysThrSerThrSerProThrArgSerMetAla
361   CCTGGGAATGCAAGCAGGGATGCAGTGCAGTCTGCACGTCCACGTCCACCCCGGAGTATGGCC

141   ProGlyAlaValHisLeuProGlnProSerThrArgSerGlnHisThrGlnProSer
421   CCAGGGGCAGTACACTTACCCCCAGCCAGTGTCCACACGCAGCCAAGT
```

FIGURE 4B

```
161  ProGluProSerThrAlaProSerThrPheLeuLeuProMetGlyProSerProPro
481  CCAGAACCCAGCCACTGCTCCAAGCACCTCCTTCCTGCTCCCAATGGGCCCCAGCCCCCA

181  AlaGluGlySerThrGlyAspPheAlaLeuProValGlyLeuIleValGlyValThrAla
541  GCTGAAGGGGAGCACTGGCGACTTCGCTCTTCCAGTGGACTGATTGTGGGTGTGACAGCC

201  LeuGlyLeuLeuIleIleGlyValValAsnCysValIleMetThrGlnValLysLysLys
601  TTGGGTCTACTAATAATAGGAGTGGTGAACTGTGTCATCATGACCCAGGTGAAAAAGAAG

221  ProLeuCysLeuGlnArgGluAlaAlaLysValProAlaAspLysAlaArgGly
661  CCCTTGTGCCTGCAGAGAGAAGCCAAGGTGCCTGCCTCACTTGCCGATAAGGCCCGGGGT

241  ThrGlnGlyProGluGlnGlnHisLeuLeuIleThrAlaProSerSerSerSerSer
721  ACACAGGGCCCCGAGCAGCAGCACCTGCTGATCACAGCCGCCTCCAGCAGCAGCAGCTCC

261  LeuGluSerSerAlaSerAlaLeuAspArgArgArgAlaProThrArgAsnGlnProGlnAla
781  CTGGAGAGCTCGGCCAGTGCCGTTGGACAGAAGGGGCCCACTCGGAACCAGCCACAGGCA

281  ProGlyValGluAlaSerGlyAlaGlyGluAlaArgAlaSerThrGlySerSerAlaAsp
841  CCAGGCGTGGAGGCCAGTGGGGGCGCCGGGGAGGCCACCGGGAGCTCAGCAGAT

301  SerSerProGlyGlyHisGlyThrGlnValAsnValThrCysIleValAlaAsnValCysSer
901  TCTTCCCCTGGTGGCCATGGGACCCAGGTCAATGTCACCTGCATCGTCGTGAACGTCTGTAGC
```

FIGURE 4C

```
321   SerSerAspHisSerSerGlnCysSerSerSerThrMetGlyAspThrAsp
961   AGCTCTGACCACACAGCTCCACAGTGCTCCTCCCAAGCCAGCAGTCCACAATGGGAGACACAGAT

341   SerSerProSerGluSerProLysAspGluGlnValProPheSerLysGluCysAla
1021  TCCAGCCCCCTCGGAGTCCCCGAAGGACGAGCAGGTCCCCCTTCTCCAAGGAGGAATGTGCC

361   PheArgSerGlnLeuGluThrProGluThrLeuLeuGlySerThrGluLysProLeu
1081  TTTCGGTCACAGCTGGAGACGCCAGAGACCCTGCTGGGGAGCACCGAAGAGAAGCCCCTG

381   ProLeuGlyValProAspAlaGlyMetLysProSer
1141  CCCCTTGGAGTGCCTGATGCTGGGATGAAGCCCAGTTAACCAGGCCGGTGTGGGCTGTGT
1201  CGTAGCCAAGGTGGCCAGGCCCTGGAGCCCTGGCCAGGATGACCCCTGCGAAGGGCCCTGGTCCTGTCCTTCCA
1261  GGCCCCCACCACTAGGACTCTGAGGCTCTTCCTGGGCCAAGTTCCTCTAGTGCCCTCCAC
1321  AGCCCGCAGCCCTCCCTCTGACCCTGCAGGCCAAGAGCCAGCGAGTTGTGGAAAGCCCT
1381  CTGCTGCCATGGCCTGTCCCCTCTCGGAAGGCTGGGCTGGCTGCCCAGCTGCACCTGGCTT
1441  GGGGCAAGTCCCCTGGGTTTTTGTTTGTTTGTTTGTTTCTCCCCGGGC
1501  CTGGAGCCCCTTGGGTTTGTTTGTTTGTTTGTTTGTTTCTCCCCCGGGC
1561  TCTGCCCAGCTCTGGCTTCCAGAAACCCCAGCATCCTTTCTGCAGAGGGCTTTCTGG
1621  AGAGGAGGGGATGCTGCCTGAGTGCTTGGAAAGCATCACCCATGAAGACAGGAGGAGGAACG
1681  AGACTGCGGGATGGTCCTGGGGCTCTGTGCAGGGAGGTGGCAGCCCTGTAGGGAACG
1741  GGGTCCTTCAAGTTAGCTCAGGAGGCTTGGAAAGCATCACCCTCAGGCCAGTGCAGTGGC
1801  TCACGCCTATGATCCCAGCACTTTGGGAGGCTGAGGCGGGTGGATCACCTGAGGTTAGGA
1861  GTTCGAGACCAGCCTGGCCAACATGGTAAAACCCCATCTCTACTAAAAATACAGAAATTA
```

FIGURE 4D

```
1921  GCCGGGGCGTGGTGGGGCCACCTATAGTCCCAGCTACTCAGAAGCCTGAGGCTGGGAAAT
1981  CGTTTGAACCCGGGAAGCCGGAGGTTGCAGGGAGCCGAGATCACGCCACTGCACTCCAGCC
2041  TGGGCGACAGAGCGAGAGTCTGTCTCAAAAGAAAAAAGCACCGCCTCCAAATGCT
2101  AACTTGTCCTTTGTACCATGGTGTGAAAGTCAGATGCCCAGAGGGCCCAGGCAGGCCAC
2161  CATATTCAGTGCTGGCCTGGGCAAGATAAACGCACTTCTAACTAGAAATCTGCCAATTT
2221  TTTAAAAAGTAAGTAACCACTCAGGCCAACAGCCAACAAAGCCAAACTCTGCCAGC
2281  CACATCCAACCCCCCACCCTGCCATTTGCACCCTCCGCCCTTCACTCCGGTGTGCCTGCAG
```

```
  1    MAPVAVWAAL  AVGLELWAAA  HALPAQVAFT  PYAPEPGSTC  RLREYYDQTA
                                                    *
 51    QMCCSKCSPG  QHAKVFCTKT  SDTVCDSCED  STYTQLWNWV  PECLSCGSRC
           * *               *           *    *              *    *    *
101    SSDQVETQAC  TREQNRICTC  RPGWYCALSK  QEGCRLCAPL  RKCRPGFGVA
                *           * *            *          * *            *
151    RPGTETSDVV  CKPCAPGTFS  NTTSSTDICR  PHQICNVVAI  PGNASMDAVC
               *    *         ‗‗‗‗‗     *          *    ‗‗‗        *
201    TSTSPTRSMA  PGAVHLPQPV  STRSQHTQPT  PEPSTAPSTS  FLLPMGPSPP

251    AEGSTGD⌐FAL  PVGLIVGVTA  LGLLIIGVVN  CVIMTQV┐KK  PLCLQREAKV
                └                             ┘          *
301    PHLPADKARG  TQGPEQQHLL  ITAPSSSSSS  LESSASALDR  RAPTRNQPQA

351    PGVEASGAGE  ARASTGSSDS  SPGGHGTQVN  VTCIVNVCSS  SDHSSQCSSQ
                              ‗‗‗‗‗‗  *            *               *
401    ASSTMGDTDS  SPSESPKDEQ  VPFSKEECAF  RSQLETPETL  LGSTEEKPLP
                                         *
451    LGVPDAGMKP  S
```

FIGURE 5

FIGURE 6A

```
1    S  D  T  V  C  D  S  C  E  D  S  T  Y  T  Q  L  W  N  W  V
1    tcggacaccgtgtgtgactcctgtgaggacagcacatacacccagctctggaactgggtt
                        10          20          30          40          50

21   P  E  C  L  S  C  G  S  R  C  S  S  D  Q  V  E  T  Q  A  C
61   cccgagtgcttgagctgtggcagctgtcccgctctgagctctgaccagctggaaactcaagcctgc
                        70          80          90          100         110

41   T  R  E  Q  N  R  I  C  T  C  R  P  G  W  Y  C  A  L  S  K
121  actcgggaacagaaccgcatctgcacctgcaggcccgggtactgtgctctgcgctgagcaag
                        130         140         150         160         170

61   Q  E  G  C  R  L  C  A  P  L  P  K  C  R  P  G  F  G  V  A
181  caggaggggtgccgcctgtgcgccccgctgcccaagtgccgcccgggcttcggcgtggcc
                        190         200         210         220         230

81   R  P  G  T  E  T  S  D  V  V  C  K  P  C  A  P  G  T  F  S
241  agaccaggaactgaaacatcagacgtggtgtgcaagccctgtgccccggggacgttctcc
                        250         260         270         280         290

101  N  T  T  S  S  T  D  I  C  R  P  H  Q  I  C  N  V  V  A  I
301  aacacgacttcatccacggatatttgcaggccccaccagatctgtaacgtggtggccatc
                        310         320         330         340         350
```

FIGURE 6B

```
121  P   G   N   A   S   R   D   A   V   C   T   S   P   T   R   S   M   A
361  cctgggaatgcaagcaggggatgcagtctgcagtccacgtccccaccggtatggcc
361                                390                400                410

141  P   G   A   V   H   L   P   Q   P   V   S   T   R   S   Q   H   T   Q   P   S
421  ccaggggcagtacacttaccccagccagtgtccacacgatcccaacacacgcagccagt
421                430                440                450                460                470

161  P   E   P   S   T   A   P   S   T   S   F   L   L   P   M   G   P   S   P   P
481  ccagaacccagcacactgctccaagcacctcctcctgctccccatgggccccagcccccca
481                490                500                510                520                530

181  A   E   G   S   T   G   D   F   A   L   P   V   G   L   I   V   G   V   T   A
541  gctgaaggggagcactggcgacttcgctcttccagttggacttgattgtgggtgtgacagcc
541                550                560                570                580                590

201  L   G   L   I   I   G   V   V   N   C   V   I   M   T   Q   V   K   K   K
601  ttgggtctactaataataggagtgtgaactgtgtcatcatgacccaggtgaaaagaag
601                610                620                630                640                650

221  P   L   C   L   Q   R   E   A   K   V   P   H   L   P   A   D   K   A   R   G
661  ccctttgtgcctgcagagagaagccaaggtgcctcacttgcctgccgataaggcccgggggt
661                670                680                690                700                710
```

FIGURE 6C

```
241 T   Q   G   P   E   Q   Q   H   L   L   I   T   A   P   S   S   S   S   S
721 acacagggccccgagcagcagcacctgctgatcacagcgcccagcagcagctcc
721               730       740       750       760       770

261 L   E   S   S   A   S   A   L   D   R   R   A   P   T   R   N   Q   P   Q   A
781 ctggagagctcggccagtgccgttggacagaagggcgcccactcggaaccagccacaggca
781               790       800       810       820       830

281 P   G   V   E   A   S   G   A   G   E   A   R   A   S   T   G   S   S   A   D
841 ccaggcgtgggaggccagtgggggccgggggccgcagccccagcgccaccgggagctcagcagagat
841               850       860       870       880       890

301 S   S   P   G   G   H   G   T   Q   V   N   V   T   C   I   V   N   V   C   S
901 tcttcccctggtggccatgggaccccaggtcaatgtcacctgcatcgtgaacgtctgtagc
901               910       920       930       940       950

321 S   S   D   H   S   Q   C   S   S   Q   A   S   S   T   M   G   D   T   D
961 agctctgaccaccacagctcctcccagccagccagctcctccacaatgggagacacagat
961               970       980       990       1000      1010

341 S   S   P   S   E   S   P   K   D   E   Q   V   P   F   S   K   E   C   A
1021 tccagccctcggagtcccccgaaggacgaggcaggtccccctttctccaaggaatgtgcc
1021              1030      1040      1050      1060      1070
```

FIGURE 6D

```
361   F   R   S   Q   L   E   T   P   E   T   L   L   G   S   T   E   E   K   P   L
1081  tttcggtcacagctggagacgccagagaccctgctggggagcaccgaagagaagcccctg
1081        1090      1100      1110      1120      1130

381   P   L   G   V   P   D   A   G   M   K   P   S
1141  cccccttggagtgcctgatgctgctggggatgaagcccagttaaccaggccggtgtgggctgtgt
1141        1150      1160      1170      1180      1190
1201  cgtagccaggtggctgagccctggcaggccctgaccctgcgaaggggccctgctccttcca
1201        1210      1220      1230      1240      1250
1261  ggccccaccactaggactctgaggctctttctggccaagtcctctagtgcccctccac
1261        1270      1280      1290      1300      1310
1321  agccgcagcctccctctgacctgcaggccaagagagcaggcagagttgtggaaagcct
1321        1330      1340      1350      1360      1370
1381  ctgctgccatggcgtgtccctctcggaaggctgggcatggacgttcggggcatgct
1381        1390      1400      1410      1420      1430
1441  ggggcaagtccctgagtctctgtgacctgccccagctgcacctgccagcctggctt
1441        1450      1460      1470      1480      1490
1501  ctggagccctgggtttttgttttgtttgtttttgtttctcccccctgggc
1501        1510      1520      1530      1540      1550
1561  tctgcccagtctctggcttccagaaacccagcatccttttctgcagaggggctttctgg
1561        1570      1580      1590      1600      1610
1621  agaggagggatgctgcctgagtcaccatgctcagtgcttcaggcctgaggctg
1621        1630      1640      1650      1660      1670
```

FIGURE 6E

```
1681   agactgcgggatggtcctggggctctgtgcaggaggaggtggcagccctgtagggaacg
1681                     1690      1700      1710      1720      1730

1741   gggtcccttcaagttagctcaggaggcttggaaagcatcacctcaggccaggtgcagtggc
1741         1750      1760      1770      1780      1790

1801   tcacgcctatgatcccagcactttgggaggctgaggcgggtggatcacctgaggttagga
1801         1810      1820      1830      1840      1850

1861   gttcgagaccagcctggccaacatggtaaaaccccatctctactaaaatacagaaatta
1861         1870      1880      1890      1900      1910

1921   gccgggcgtggtggcgggcacctatagtcccagctactcagaagcctgaggctgggaaat
1921         1930      1940      1950      1960      1970

1981   cgtttgaacccgggaggcggaggttgcaggagccgagatcacgccactccagcc
1981         1990      2000      2010      2020      2030

2041   tgggcgacagagagcgagagtctgtctcaaaagaaaaaaagcaccgcctccaaatgct
2041         2050      2060      2070      2080      2090

2101   aacttgtcctttgtaccatggtgtgaaagtcagagtcagatgcccagaggggccaggccac
2101         2110      2120      2130      2140      2150

2161   catattcagtgctgtggcctgggcaagatcaacgcacttctaactagaaatctgccattt
2161         2170      2180      2190      2200      2210

2221   tttaaaaaagtaagtaccactcaggccaacaagccaacgacaaagccaaactctgccagc
2221         2230      2240      2250      2260      2270

2281   cacatccaaccccaccctgccatttgcaccctccgccttcactccggtgtgctgcag
2281         2290      2300      2310      2320      2330
```